



SEQUENCE LISTING

<110> KATO, Seishi
KIMURA, Tomoko

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 2003-0984/WMC/01791

<140> 10/019,151
<151> 2002-08-20

<150> PCT/JP00/03944
<151> 2000-06-16

<150> JP 11-178065
<151> 1999-06-24

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Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr
35 40 45
Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val
50 55 60
Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu
65 70 75 80
Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
85 90 95
Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
100 105 110
Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
115 120 125
Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His
130 135 140
Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
145 150 155 160
Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
165 170 175
Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile
180 185 190
Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala
195 200 205

Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly
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Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
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<213> Homo sapiens

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35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180 185 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210 215 220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225 230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
260 265 270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
 275 280 285
 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
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 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
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 325 330 335
 Arg Arg Arg

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 35 40 45
 Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser
 50 55 60
 Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn
 65 70 75 80
 Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly
 85 90 95
 Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys
 100 105 110
 Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp
 115 120 125
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 130 135 140
 Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys
 145 150 155 160
 Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly
 165 170 175
 Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala
 180 185 190
 Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr
 195 200 205
 Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala
 210 215 220

Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
 225 230 235 240
 Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro
 245 250 255
 His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
 260 265 270
 Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
 275 280 285
 Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly
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 Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser
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 Val Glu Glu Glu Gln Cys
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 35 40 45
 Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu
 50 55 60
 Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr
 65 70 75 80
 Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala
 85 90 95
 Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys
 100 105 110
 Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr
 115 120 125
 Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser
 130 135 140
 Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr
 145 150 155 160
 Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
 165 170 175
 Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
 180 185 190
 Val Gln Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys

195	200	205													
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210						215									220
Pro	Gln	Lys	Lys	Trp	Leu	His	Phe	Ile	Ser	Pro	Ile	Phe	Val	Gln	Ala
225					230				235						240
Leu	Thr	Leu	Thr	Phe	Leu	Ala	Glu	Trp	Gly	Asp	Arg	Ser	Gln	Leu	Thr
							245		250					255	
Thr	Ile	Val	Leu	Ala	Ala	Arg	Glu	Asp	Pro	Tyr	Gly	Val	Ala	Val	Gly
							260		265					270	
Gly	Thr	Val	Gly	His	Cys	Leu	Cys	Thr	Gly	Leu	Ala	Val	Ile	Gly	Gly
						275		280					285		
Arg	Met	Ile	Ala	Gln	Lys	Ile	Ser	Val	Arg	Thr	Val	Thr	Ile	Ile	Gly
290						295						300			
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Asp Ser Gly Phe

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<213> Homo sapiens

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Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val	
					35			40					45			
Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu	
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His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala	
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Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Val	Gln	Phe	Thr	
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Ala	Ser	Arg	Lys	Phe	Leu	Thr	Ile	Thr	Pro	Ile	Val	Leu	Tyr	Phe	Leu	
					100			105					110			
Thr	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Gln	Ile	His	Phe	Val	Leu	Asn	Thr	
					115			120					125			
Val	Ser	Leu	Met	Ser	Val	Leu	Ile	Pro	Lys	Leu	Pro	Gln	Leu	His	Gly	
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35 40 45
Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu
50 55 60
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
65 70 75 80
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr
85 90 95
Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu
100 105 110
Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr
115 120 125
Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly
130 135 140
Val Arg Val Phe Gly Ile Asn Lys Tyr
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<213> Homo sapiens

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Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe
35 40 45
Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg
50 55 60
Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu
65 70 75 80
Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val
85 90 95
Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe
100 105 110
Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser
115 120 125

Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val
 130 135 140
 Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys
 145 150 155 160
 Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met
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 Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr
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 Leu Glu Lys Thr Ile His Glu Glu
 195 200

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 <213> Homo sapiens

<400> 8
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 35 40 45
 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
 50 55 60
 Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
 65 70 75 80
 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
 85 90 95
 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
 100 105 110
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
 115 120 125
 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 130 135 140
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
 145 150 155 160
 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
 165 170 175
 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
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gatttggtt	cctatcttaa	aactcgatca	ccagtcacct	tcctgtctga	tctgcgcagc	180
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gtgctctatg	tcgggactca	ggccattgcg	cacatccaca	acaaggcag	cacacctca	300
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gacactgagg	gtcgctatct	cttttgaat	gcaattgcaa	atcagctccg	gtacccaaat	420
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aaccatgaat	ttgtacactg	tgccccagaa	atcgaaaatg	tattccagtc	ggtcgcacag	660
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<212> DNA

<213> Homo sapiens

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atacagtgtc	agaacaaagg	ctgggatggg	tatgatgtac	agtgggaatg	taagacggac	300
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ggcacgtgaa	atagggctta	ctcacccctt	catggaggct	cgggcagct	ttcggtatgt	960
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<210> 11

<211> 978

<212> DNA

<213> Homo sapiens

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ggcacacaga	aggtgccc	gccccgtgc	gagaaaggc	tggcagccaa	gtgctttgac	180
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cagtatcata	atcagccat	ccactctgtc	tctgagggg	tcgacttcta	ctccgagctg	900
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caccgaaaca aagaaccggc ggcggccggcc cagcagctgc agccgcagcc tggctgtg 180
cagggccccc agccggcccg ggtcgagaaa atatttacac cagcagctcc agttcatacc 240
aataaagaag atccctgtac ccaactaat ttgggattta tccatgcatt tgcgtgtcc 300
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gatgaagaat ttcaacgaac caaactttt aatggaccgg gagatgttga aacgggtaca 660
agcataacag tacctcagaa aaagtgggtt cattttattt caccatccc tgttcaagct 720
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gcagcttagag aggaccctt tggtagcc gttgggtggaa ctgtggggca ctgcctgtc 840
acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg 900
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<212> DNA
<213> Homo sapiens

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ttcttgacca tcacacccat cgtctgtac ttccctcacca gcttctacac taagtacgac 360
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<210> 14
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cccttcttca gcatttctgt tgcacacggc ctgaccaacg tcattccatcaa cctggctacg 180
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<212> DNA
<213> Homo sapiens

<400> 15

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ttcctgttca gacgctgctt caaggtaaa catgatgctt tgaagacata tgc当地 240
gctacactt cattttgtc tactgttggt actgacaagc tttttgtat tgatgcttt 300
tattcagata atataagcaa ggaaaactgt gttttcagaa gctcaactgtat tggcatagtt 360
tgtgggttt tctatccc当地 ttcttggct tttactaaaa atggacgc当地 ggcaaccaag 420
tatcataccg ttccactgccc accaaaagga agggttt当地 tccattggat gacgcttt 480
caaacacaaa tggaaattat ggc当地 ttagtcttc agattatgtt tggatattt 540
aatggtctat accattatgc agtattt当地 gagacactt当地 agaaaactat acatgaagag 600

<210> 16

<211> 567

<212> DNA

<213> Homo sapiens

<400> 16

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tcagccaca tggccgctca cctgc当地 gatgc当地 gagctgtggc ttaccagatg 180
tggcaaaatc tggcaaaagc agagacaaa cttcatatc当地 caaactctgg ggggc当地 240
gagctgagcg agttggtca cacgatgctc ctggaccggg gctgctccg gaactggcag 300
gactacggg ttc当地 gagaagt ggaccaagtg aaacgtctca caggccc当地 acttagcgag 360
gggccc当地 caagcatcag cgtgatggc当地 acagggggccc当地 cctggccctac caggctctcc 420
aggacatgtt tgc当地 acttctt当地 gggggagttt ggagaagacc agatctatga agccc当地 480
caaggccc当地 gggctctgg当地 ggc当地 attgctta tttgggggacccc当地 cttggccctac cttggccctac 540
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<210> 17

<211> 1167

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (187) ... (903)

<400> 17

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ttcttctaaa gaaagaaaaga ctgat当地 aatgtggca gctgtctt当地 tcaaggcatt 120
tatagtgtat atagtttag aaaaacagtc ccaccactt当地 agcatagatg taat当地 180
ataaaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228
Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val
1 5 10
gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276
Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe
15 20 25 30
act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324
Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu
35 40 45
aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372
Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu
50 55 60
cag gca tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420
Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn
65 70 75
gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac 468
Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn
80 85 90
aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516
Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met
10

95	100	105	110	
gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat				564
Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr				
115	120	125		
ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac				612
Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His				
130	135	140		
act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat				660
Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn				
145	150	155		
acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg				708
Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu				
160	165	170		
att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag				756
Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu				
175	180	185	190	
ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac				804
Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His				
195	200	205		
tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc				852
Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys				
210	215	220		
atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt				900
Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser				
225	230	235		
tagacgaaac tgcacatctctg ttgtacgtgt cagtcttagag gtctcactgc accgagttca				960
taaactgact gaagaatcct ttcaacgtctt cctgactttc ccagcccttt gggtttgtggg				1020
tatctgcccc aactactgtt gggatcagcc tcctgtctta tggggcacg ttccaaagtt				1080
taaaatgcatt ttttgactc ttggccaaaa tttagaaagat gctgtgaata tcattttgaa				1140
cttgcgtaaa tacatgaaag agaaaaac				1167

<210> 18
<211> 1925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (115)... (1134)

<400> 18				
gttccttcgc cgccgccagg ggttagcggtg tagctgcgcg cgcgtcgccg cgctaccgca	60			
cccaggttcg gccccgttaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg		117		
Met				
1				
gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc				165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly				
5	10	15		
ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac				213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp				
20	25	30		
cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat				261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr				
35	40	45		
gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa				309
Asp Arg Tyr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys				
50	55	60	65	
tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata				357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile				
70	75	80		
cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt				405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys				
85	90	95		

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc	453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser	
100 105 110	
tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct	501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser	
115 120 125	
tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa	549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys	
130 135 140 145	
ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat	597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr	
150 155 160	
tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att	645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile	
165 170 175	
acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc	693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe	
180 185 190	
ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca	741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro	
195 200 205	
ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc	789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro	
210 215 220 225	
cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggr cat ggt	837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly	
230 235 240	
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa	885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu	
245 250 255	
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta	933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu	
260 265 270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg	981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser	
275 280 285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg	1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg	
290 295 300 305	
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca	1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser	
310 315 320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg	1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg	
325 330 335	
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaaatt ttggatttt	1180
Arg Arg	
tcatcacttt ctcttttagaa aaaaagtact acctgttaac aattggaaaa aggggatatt	1240
caaaaagttct gtgggtttat gtccagtgtat gctttttgtat ttcttattatt tgaggctaaa	1300
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt	1360
gcagttttg aaagtgtatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct	1420
gtgatgccct aagaagcatt aagaatgaag gtgttgact aatagaaaact aagtacagaa	1480
aatttcagtt ttaggtgggtt gtagctgtatg agttattacc tcatagagac tataatattc	1540
tatttggat tatattattt gatgtttgtt gttcttcaaa catttaaattc aagctttgga	1600
ctaattatgc taatttgtga gttctgtatca cttttgagct ctgaagcttt gaatcattca	1660
gtgggtggaga tggccttctg gtaactgtaat attaccttct gttaggaaaag gtggaaaaata	1720
agcatctaga aggttgggtt gaaatgactct gtgctggcaa aaatgcttga aacctctata	1780
tttcttcgt tctataagagg taaaggtcaa attttcaac aaaagtcttt taataacaaa	1840
agcatcgatg tctctgtgaa atctcaaata ttgttgtaat agtctgtttc aatcttaaaa	1900
agaatcaata aaaacaaaca agggg	1925

<211> 1125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (71) ... (1051)

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gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109
Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln
1 5 10
cg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157
Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser
15 20 25
aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205
Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val
30 35 40 45
ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met
50 55 60
cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta 301
Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val
65 70 75
caa tac aac tgg gag act ggg gat gac cg ttc tcc ttc cgg agc ttc 349
Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe
80 85 90
cg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg 397
Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly
95 100 105
gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa 445
Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu
110 115 120 125
atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa 493
Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln
130 135 140
ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac 541
Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn
145 150 155
cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc 589
Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val
160 165 170
ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc 637
Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
175 180 185
ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
190 195 200 205
tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
210 215 220
tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
225 230 235
ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
240 245 250
tgc cta cca cat cac cat cag tgt ttc cct cg cg ctg tca agt gca 877
Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
255 260 265
gcc ccc acc gtc ggt cct ttg acc agc tac cac cag tat cat aat cag 925
Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
270 275 280 285

ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg	973
Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg	
290 295 300	
aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt	1021
Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val	
305 310 315	
agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg	1070
Arg Ser Ser Val Glu Glu Gln Cys	
320 325	
agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc	1125

<210> 20
<211> 1734
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (40) ... (1014)

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ctcttgccgc gccccgtgcgc ggccggcccg gcaggcggg atg gcg gcc gcg gct	54
Met Ala Ala Ala Ala	
1 5	
ccg gag aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg	102
Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu	
10 15 20	
gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa	150
Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu	
25 30 35	
gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg	198
Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu	
40 45 50	
cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag	246
Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu	
55 60 65	
aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct	294
Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro	
70 75 80 85	
gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata	342
Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile	
90 95 100	
tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca	390
Ser Val Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala	
105 110 115	
gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca	438
Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala	
120 125 130	
atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat	486
Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr	
135 140 145	
gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta	534
Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val	
150 155 160 165	
tta ttt gcc att ttt ggc att aga atg ctt ccg gaa ggc tta aag atg	582
Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met	
170 175 180	
agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta	630
Ser Pro Asp Glu Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu	
185 190 195	
aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg	678
Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro	
200 205 210	

gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg	726
Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp	
215 220 225	
ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc	774
Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe	
230 235 240 245	
tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca	822
Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala	
250 255 260	
gct aga gag gac ccc tat ggt gta gcc gtc ggt gga act gtc ggg cac	870
Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His	
265 270 275	
tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag	918
Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln	
280 285 290	
aaa atc tct gtc aga act gtc aca atc ata aga ggc atc gtt ttt ttg	966
Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu	
295 300 305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt	1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe	
310 315 320	
taacgctgt ttgttcatct atatttagtt taaaatagtt agtattatct ttctgtacat	1070
agtgtacatt acaactaaaaa gtgtatggaaa aatactgtat tttagtagcac tgattttgt	1130
agtttgcacc attattatgt ctgagatata atcattgatt ctatgttcaa caaggagttt	1190
taaaagaaac ctgacttcta agtgtgggtt ttcttctct ccaacataat tatgttaata	1250
ttgtcctcat tttctttttt gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt	1310
ctttcagcac tgacccttt ttaaggaata caaatttct ccttcatcac ttaggtttt	1370
taagatgttt accttaagt tttcttggg gaaagaatga attaatttct atttcttaaa	1430
acattccct gagccagtaa acagtagttt aatcatttgc ttttcaaaa ctaggtttt	1490
aaaaaaaaagag acatatatgta tattgctgtt atatcaataa catggcacaa caagaactgt	1550
ctgccaggc attcttcctc tttttttt aattgggttag gacacccaaat ataaaaaacag	1610
tcaatattt acaatgtgga attaccaaataaaagagaa tactatgaat gtattcatat	1670
ttttctata ttgaataaaac aatgtaacat agataacaat ataaaataaaa gtggtatgac	1730
cagt	1734

<210> 21
<211> 2064
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (98) ... (559)

aaaacagctg ctggagcagc agcggccccc gctcccggga accgttcccg ggccgttcat	60
cttcggccccc acacgaacag cagaggggg cagcagg atg aat gtc ggc aca	112
Met Asn Val Gly Thr	
1 5	
gcg cac agc gag gtc aac ccc aac acg cgg gtc atg aac agc cgt ggc	160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly	
10 15 20	
atc tgg ctc tcc tac gtc ctg gcc atc ggt ctc ctc cac atc gtc ctg	208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu	
25 30 35	
ctg agc atc ccg ttt gtc agt gtc cct gtc gtc tgg acc ctc acc aac	256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn	
40 45 50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtc aag ggg	304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly	
55 60 65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac	352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His	

70	75	80	85	
tgg gag cag atg gat tat	ggg gtc cag ttc acg	gcc tct cgg aag ttc		400
Trp Glu Gln Met Asp Tyr	Gly Val Gln Phe Thr	Ala Ser Arg Lys Phe		
90	95	100		
ttg acc atc aca ccc atc	gtg ctg tac ttc ctc	acc agc ttc tac act		448
Leu Thr Ile Thr Pro Ile	Val Leu Tyr Phe Leu	Thr Ser Phe Tyr Thr		
105	110	115		
aag tac gac cag atc cat	ttt gtg ctc aac acc	gtg tcc ctg atg agc		496
Lys Tyr Asp Gln Ile His	Phe Val Leu Asn Thr	Val Ser Leu Met Ser		
120	125	130		
gtg ctt atc ccc aag ctg	ccc cag ctc cac gga	gtc cggtt att ttt gga		544
Val Leu Ile Pro Lys Leu	Pro Gln Leu His Gly	Val Arg Ile Phe Gly		
135	140	145		
atc aat aag tac tgagagtgc	cccccttcccc ctgccccaggg	tggcagggga gggg		600
Ile Asn Lys Tyr				
150				
tagggtaaaa ggcatgtgct	gcaacactga agacagaaaag	aagaagcctc tggacactgc		660
cagagatggg ggttgagcct	ctggcctaatttccccccctc	gcttccccca gtagccaact		720
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gctcacttgttgc	ttgcctcgcg cgcggccaaag	cactttaacc cctgcataagg		960
cggtagggcttgc	tttgcatttttgc	cacggcgttgc		1020
gtgcttttgtt gtagggaaagc	aagtgtggga tgggttttttgc	cctttctggg tagggagctg		1080
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tgggttaac tcctgggttgc	gctgttttttgc	agacagggttgc ggaaaaggcc		1500
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aacgtgggt gctgtggttc	tctgcaggcc ctcacccctt	aacttcctca tacagactgg		1620
caactggcag ggcctctcat	gtggcagcca catgtgggt	tgtgaggcca ccccatgtgg		1680
ggctctgtgtt gagagtccgt	taggatccct gctcaagcag	cacagaggaa gggcaagac		1740
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gggctggagc cttctccctt	cccccagtgg actaggggca	gtgttaattt tgaaaagggtg		1860
tgggtccctg tgcctcttc	cagggttcca agggAACAGG	agaggtcaact gggcctgttt		1920
tctcccttc gaccctgcatt	ctcccacccc gtgtatcata	gggaactttc accttaaaat		1980
cttcttaaagc aaagtgtgaa	taggattttt actccctttt	tacagtattt tgagaaacgc		2040
aaataaaaagg gcaacatgtt	tctg			2064

<210> 22
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (28) ... (489)

<400> 22				
agccggacgg ggatctgagc	tggcagg atg aat gtg	ggg gtg gca cac agc		51
	Met Asn Val Gly Val	Ala His Ser		
	1	5		
gaa gta aac ccc aac acc	cga gtg atg aat agc	cga ggc atc tgg ctg		99
Glu Val Asn Pro Asn Thr	Arg Val Met Asn Ser Arg	Gly Ile Trp Leu		
10	15	20		
gcc tac atc atc ttg	gta gga ttg ctg cat	atg gtt cta ctc agc atc		147
Ala Tyr Ile Leu Val	Gly Leu Leu His Met Val	Leu Leu Ser Ile		
25	30	35		
ccc ttc ttc agc att	cct gtt gtc tgg acc	ctg acc aac gtc atc cat		195
Pro Phe Phe Ser Ile	Pro Val Val Trp Thr	Leu Thr Asn Val Ile His		

aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt Asn Leu Ala Thr Tyr Val Phe Leu His Thr Val Lys Gly Thr Pro Phe 60 65 70 gag act cct gac caa gga aag gct cgg cta ctg aca cac tgg gag caa Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln 75 80 85 atg gac tat ggg ctc cag ttt acc tct tcc cgc aag ttc ctc agc atc Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile 90 95 100 tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat Ser Pro Ile Val Leu Tyr Leu Ala Ser Phe Tyr Thr Lys Tyr Asp 105 110 115 120 gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu 125 130 135 ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys 140 145 150 tac tgag ggtatgggttt tggacagct ccatggcat gggaaaggca ctgaaacaga Tyr ggactataaa acatccttct cttattctcc	45 50 55 243 291 339 387 435 483 540 570
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<210> 23
<211> 1161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (278)... (880)

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cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro 10 15 20	
atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa Met Val Ile Glu Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu 25 30 35	
atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly 40 45 50	
ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val 55 60 65	
aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe 70 75 80 85	
ttg tct act gtt act gac aag ctt ttt gta att gat gct ttg tat Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr 90 95 100	
tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile 105 110 115	
ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa	

Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys		
120 125 130		
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa	724	
Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys		
135 140 145		
gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa	772	
Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys		
150 155 160 165		
tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat	820	
Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn		
170 175 180		
ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata	868	
Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile		
185 190 195		
cat gaa gag taaccaaaaa aatgaatggt tgctaactta gcaaaatgaa gtt	920	
His Glu Glu		
200		
tctataaaga ggactcaggc attgctgaaa gagttaaaag taactgtgaa caaataattt	980	
gttctgtgcc tttgcctgg tatatagcaa atactcaaaa agtattcaat aattcaatca	1040	
ataaaatataa gtttcatctt acacgtaaga tacaggtctt atctcctgat ggtgtgtcca	1100	
ttttgcctgg tatataacag ataataaaata tccagtgta ataataatgtaa caataaaaagt	1160	
t	1161	

<210> 24
<211> 823
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (58) ... (627)

<400> 24		
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Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala		
1 5 10 15		
atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca	153	
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro		
20 25 30		
caa ctg gat gag gag atg tac tca gcc cac atg ccc gct cac ctg	201	
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu		
35 40 45		
cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg	249	
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu		
50 55 60		
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg	297	
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg		
65 70 75 80		
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc	345	
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser		
85 90 95		
cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt	393	
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg		
100 105 110		
ctc aca ggc cca gga ctt acg gag ggg cca gag cca agc atc agc gtg	441	
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val		
115 120 125		
atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg	489	
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu		
130 135 140		
cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa	537	
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln		

145	150	155	160	
caa ggc cga ggg gct	ctg gag gca ttg	cta tgt ggg gga	ccc cag ggg	585
Gln Gly Arg Gly	Ala Leu Glu Ala Leu	Leu Cys Gly	Gly Pro Gln Gly	
165	170	175		
gcc tgc tca gag aag	gtg tca gcc aca	aga gaa gag	ctc tagtcc	630
Ala Cys Ser Glu Lys	Val Ser Ala Thr	Arg Glu Glu	Leu	
180	185			
tggactctac cctcctctga	aagaagctgg ggcttgctct	gacggtctcc	actcccgct	690
gcaggcagcc aggagggcag	gaagcccttg ctctgtgt	ccatcctgcc	tccctcctcc	750
agcctcaggg cactcgggcc	tgggtggag tcaacgcctt	ccccccttgaa	ctcaaataaa	810
acccagtgac ctc				823